Webinar Instructions

Welcome to the Kids First X01 Pre-Application Webinar

- Every participant is muted upon entry.
- To ask public questions, use the **Q&A** bar (right side of your screen). We encourage you to save these for the question periods.
- You can ask also use the "chat"  service to send private messages to the host or presenters throughout the webinar.
- After the webinar, additional questions can be emailed to: valerie.cotton@nih.gov

This webinar will be recorded.
We will start at noon (EDT)

Pre-Application Webinar for

PAR-19-390, Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)

November 21, 2019

12:00 pm EST

NIH

The Common Fund

Gabriella Miller Kids First

PEDIATRIC RESEARCH PROGRAM

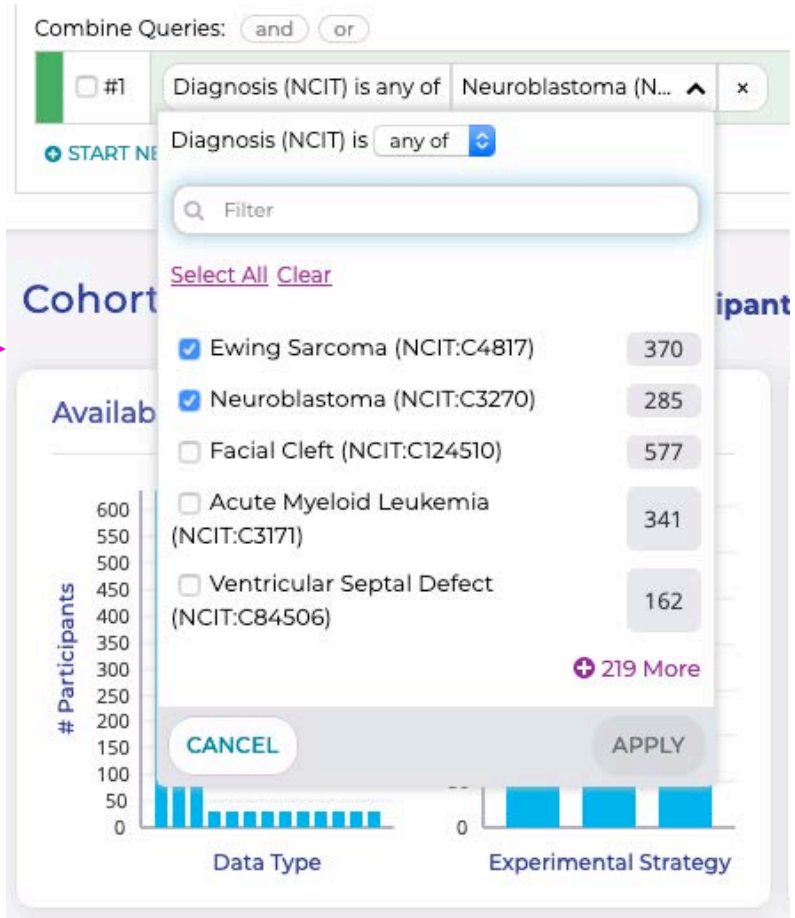
Agenda

- **12-12:25pm.** PAR-19-390 **- *Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)* –** Valerie Cotton, NICHD
- **12:25-12:30pm.** PAR-19-375- ***Small Research Grants for Analyses of Gabriella Miller Kids First Pediatric Research Data (R03 Clinical Trial Not Allowed)*** – James Coulombe, NICHD
- **12:30-12:35pm.** Common Fund FOA – Marie Nierras
- **12:35-12:45pm.** ORIP FOAs – Sige Zou & Oleg Mirochnitchenko
- **12:45-12:55pm.** NIDCR FOAs – Emir Khatipov
- **12:55-1pm.** Questions & Additional FOAs

Watch the Fall Public Webinar from September 26th

https://youtu.be/NDatoQxvLKo

- Introduction by NIH Kids First staff (~5min)
- New Kids First Data Resource Portal Features – DRC (~30min)
- Kids First X01 Neuroblastoma Project Findings – Sharon Diskin, PhD (~30min)
- Kids First Program Updates – NIH (~15min)
- Kids First Second Chance – NIH (~10min)
- Questions (~15min)



Vision

Alleviate suffering from childhood cancer and structural birth defects by fostering **collaborative research** to uncover the etiology of these diseases and supporting **data sharing** within the pediatric research community.

NIH Kids First Working Group

Kids First is an NIH Common Fund program coordinated by a **trans-NIH Working Group**, which is chaired by four institutes:

- *Eunice Kennedy Shriver* National Institute of Child Health and Human Development (**NICHD**)
- National Human Genome Research Institute (**NHGRI**)
- National Heart, Lung, and Blood Institute (**NHLBI**)
- National Cancer Institute (**NCI**)

The Common Fund

Other Working Group Representation:

NIDCR	**NIAAA**	**NIDDK**	**NEI**	**NIAID**	**ORIP**
NIDA	**NINDS**	**NIEHS**	**NIAMS**	**NCATS**	**CDC**

https://commonfund.nih.gov/kidsfirst/members

Kids First Major Initiatives

$12.6 million per year for 10 years, pending appropriations

Year	15	16	17	18	19	20	21	22	23	24

Cohort identification & DNA sequencing

- Identify children with cancer and/or structural birth defects, and their families (X01)
- Whole genome sequencing by the Kids First Sequencing Centers

Data Resource Center

- Develop a resource of well-curated clinical and genetic sequence data to facilitate and empower genomic discovery
- Provide computational infrastructure and analysis tools to interrogate large and complex datasets

Kids First X01 Cohorts (Years 1-4)

Disorders of Sex Development (FY15)
Congenital Diaphragmatic Hernia (FY15, 16, 17)
Ewing Sarcoma (FY15, 17)
Orofacial Clefts; Caucasian (FY15), Latin American (FY16), Asian & African (FY17)
Osteosarcoma (FY15)
Structural Heart & Other Defects (FY15, 16, 18)
Syndromic Cranial Dysinnervation Disorders (FY15)
Cancer Susceptibility (FY16)
Adolescent Idiopathic Scoliosis (FY16)
Familial Leukemia (FY16)
Hearing Loss (FY16)
Neuroblastomas (FY16)
Craniofacial Microsomia (FY17)
Enchondromatoses (FY17)
Hemangiomas, Vascular Anomalies & Overgrowth (FY17, 18)
Nonsyndromic Craniosynostosis (FY17)
Patients with both childhood cancer and birth defects (FY17)
Bladder Exstrophy (FY18)
Cornelia de Lange Syndrome (FY18)
Esophageal Atresia and Tracheoesophageal Fistulas (FY18)
Kidney and Urinary Tract Defects (FY18)
Intracranial Germ Cell Tumors (FY18)
Microtia (FY18)
Fetal Alcohol Spectrum Disorders (FY18)
Myeloid Malignancies + overlap with Down syndrome (FY18)
Congenital Heart Defects and Acute Lymphoblastic Leukemia in Children with Down Syndrome (FY18)

- **26 projects**
- **~10,000 patients** (+ family members and tumors)
- **4 X01 cycles**
- **8 released datasets**

2019 X01 Cohorts (Year 5)

Structural Brain Defects
Structural Defects of the Neural Tube (Spina Bifida: Myelomeningocele)
Orofacial Clefts in the Philippines
CHARGE Syndrome
Laterality Birth Defects
Kidney and Urinary Tract Defects
Esophageal Atresia & Tracheoesophageal Fistulas
Congenital Anomalies of the Kidney & Urinary tract
T-cell Acute Lymphoblastic Leukemia
Pediatric Rhabdomyosarcoma
Extracranial Germ Cell Tumors

> 10,000 genomes

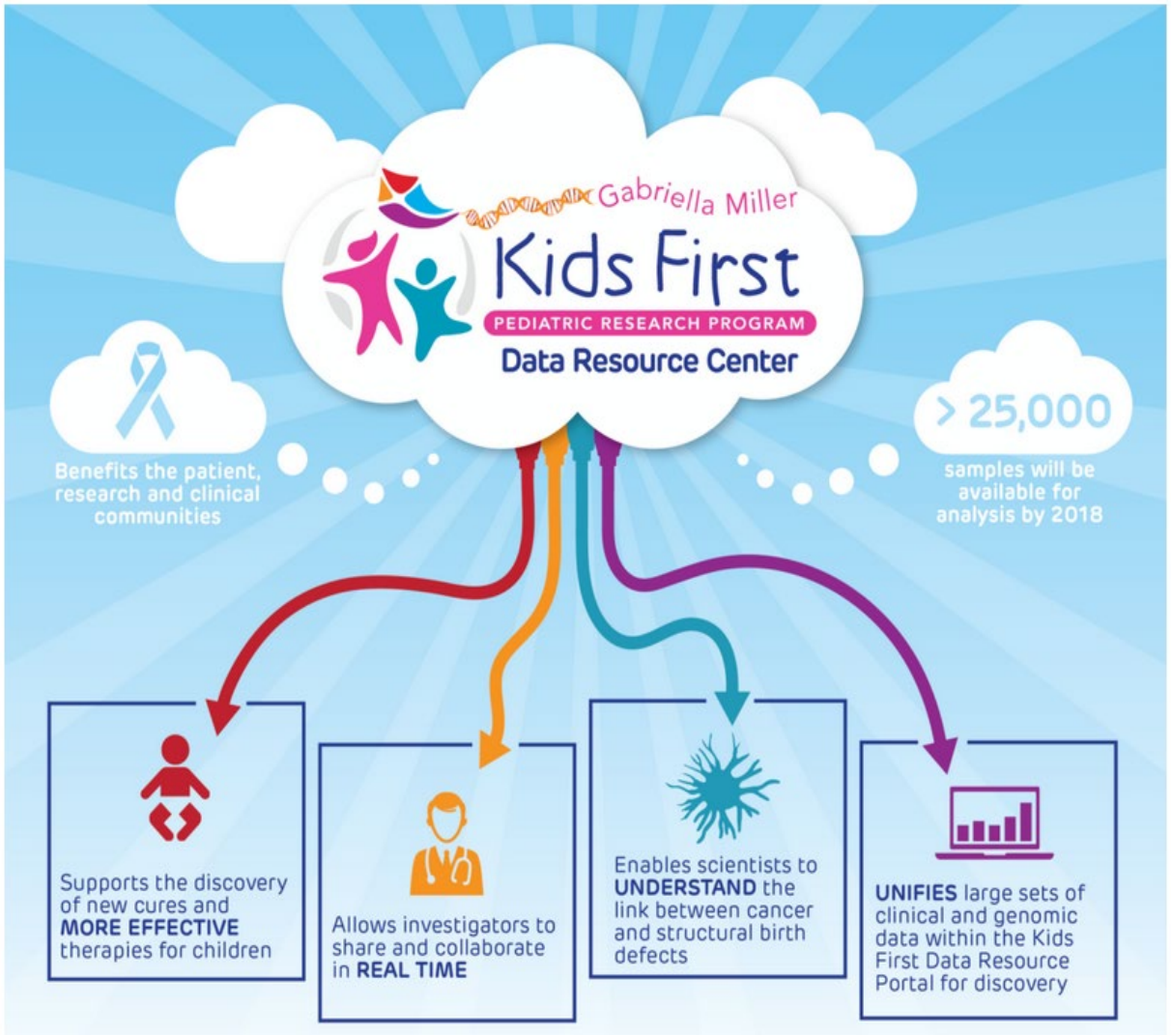
BROAD INSTITUTE

HUDSONALPHA INSTITUTE FOR BIOTECHNOLOGY

St. Jude Children's Research Hospital

Abstracts & Contact PIs listed on: https://commonfund.nih.gov/kidsfirst/x01projects

Data Resource Center (DRC)



D3b Center for Data-Driven Discovery in Biomedicine

Children's Hospital of Philadelphia℠

SevenBridges genomics

OICR Ontario Institute for Cancer Research | IORC Institut ontarien de recherche sur le cancer

THE UNIVERSITY OF CHICAGO

OHSU OREGON HEALTH & SCIENCE UNIVERSITY

Children's National Health System

Kids First Data Resource Center

Gabriella Miller Kids First
PEDIATRIC RESEARCH PROGRAM
Data Resource Center

Data Coordination Center

- Clinical & phenotypic data harmonization using ontologies
- Genomic data harmonization against latest reference build with an optimized and scalable pipeline

Administration & Outreach

- Coordinate and communicate across the DRC
- Engage the broader community including researchers, physicians, patients, and foundation advocates

Data Resource Portal

- Develop interface to enable users of all skill levels to browse, visualize, and analyze across Kids First and related data
- Develop analytic frameworks and cloud-based workspaces to enable collaborative analysis and empower research

PAR-19-390 (FY20)

Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)

2020 X01: 6th Cycle

Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)

1. FY 2015: PAR-15-259
   - 2 childhood cancer projects
   - 5 structural birth defects projects
2. FY 2016: PAR-16-150
   - 3 childhood cancer projects
   - 5 structural birth defects projects
3. FY 2017: PAR-17-063
   - 2 childhood cancer projects
   - 5 structural birth defects projects
   - 1 projects with overlap of structural birth defects and childhood cancer
4. FY 2018: PAR-18-583
   - 2 childhood cancer projects
   - 7 structural birth defects projects
   - 2 projects with overlap of structural birth defects and childhood cancer
5. FY 2019: PAR-19-104
   - 3 childhood cancer projects
   - 7 structural birth defects projects
6. **FY 2020: PAR-19-390**

X01 mechanism

- Not an “award”; Recipients are selected for the opportunity to have their cohort sequenced by Kids First sequencing centers and data shared through the Kids First Data Resource
- No Notice of Award; Kids First can provide a letter acknowledging and explaining that your project was selected for the X01 program
- Not listed in the NIH RePORTER
  - Abstracts and X01 information listed on Kids First website: https://commonfund.nih.gov/kidsfirst/fundedresearch
- No funds, but can apply for other grants (e.g. Kids First R03) to support analysis of X01 project.

X01 Selection Considerations

Following **scientific peer review**, Kids First program officers evaluate projects based on the following factors, and selections are finalized by Kids First Working Group Co-Chairs.

- Scientific and technical merit (determined by scientific peer review).
- Value of incorporating the dataset into the Data Resource to empower research among the pediatric research community.
- Balance of childhood cancers and birth defects; conditions not previously sequenced will be prioritized.
- Broad data sharing and use
- Informative study design and sufficient clinical and phenotypic data.
- Availability of samples in timely manner.
- Sample quality in terms of suitability for whole genome sequencing (as well as exome and RNASeq if applicable).

Data Flow

The Kids First DRC is charged with:

- re-processing and “harmonizing” data generated by the sequencing centers to facilitate analyses across all Kids First datasets
- providing a central portal where these data and analysis tools will be readily accessible to the research community

Phenotypic data →
Sequence data →

→

X01 Recipients

Pediatric Research Community

X01 investigators are encouraged to utilize and work collaboratively with the Kids First Data Resource Center to pursue specific analyses. Visit: kidsfirstdrc.org

dbGaP & the DRC

Data is made accessible through dbGaP & Kids First Data Resource Center (DRC)

- While the Data Resource is the NIH designated repository for Kids First data, all Kids First projects are registered, authenticated, and approved through dbGaP
- All dbGaP Data Access Requests (DARs) will be processed by **the Kids First Data Access Committee** run by the NCI Office of Data Sharing

Kids First
Data Access Committee
(NIH)

PAR-19-390
Goals & Expectations

Overall Goal

Identify a diversity of childhood cancer and structural birth defects cohorts to generate high quality and broadly shareable and usable genomic datasets that will be of high value to the pediatric research community.

Sequencing

<u>Goal</u>: Generate high quality whole genome sequence and variant data from childhood cancer and structural birth defects cohorts.

WGS, whole exome sequencing (WES), and RNA sequencing may be available for tumor or affected tissue, when justified.

<u>Expectations</u>:

- DNA extractions must be of sufficient quality and concentration for WGS (and/or WES).
- RNA extractions (for tumor/affected tissue) must be of sufficient quality and concentration for RNASeq.
- Extractions will be ready to ship shortly after selection

Sequencing

Sequencing Centers perform sequencing & variant calling
Generate CRAM/BAM & VCF files

- **Germline/Normal**: WGS at 30X coverage (NovaSeq)
- **Tumor or Affected tissue** (when available):
  - HudsonAlpha St Jude: 30X WGS + 100X WES + 100X RNASeq
  - Broad: 90X WGS, RNASeq

- *You may propose other approaches (e.g., higher coverage or complementary exome sequencing).*
- *Project design will be finalized in discussions among the X01 investigators, the sequencing centers, and NIH program staff*

Volume/Concentration Recommendations

Can be found on our FAQ page: https://commonfund.nih.gov/kidsfirst/FAQ

Amount of DNA/RNA and coverage

	Amount DNA or RNA required/recommended	Concentration	Coverage	Additional info.
WGS	~2ug DNA	20-50 ng/ul preferred	30X	paired end reads
WES	275 ng DNA (minimum); 1 ug recommended	20 ng/ul (minimum)	100X, greater than 80% coding exons covered at 20X	paired end reads
RNA-Seq	750 ng total RNA (minimum); 1 ug recommended	20 ng/ul (minimum)	100X, greater than 40% coding exons covered at 20X	paired end reads

Data Sharing

Goals:

1. **Make data generated by Kids First as accessible and usable as possible to the research community.**
2. **Enable researchers to easily combine/compare datasets for cross-disease analyses.**

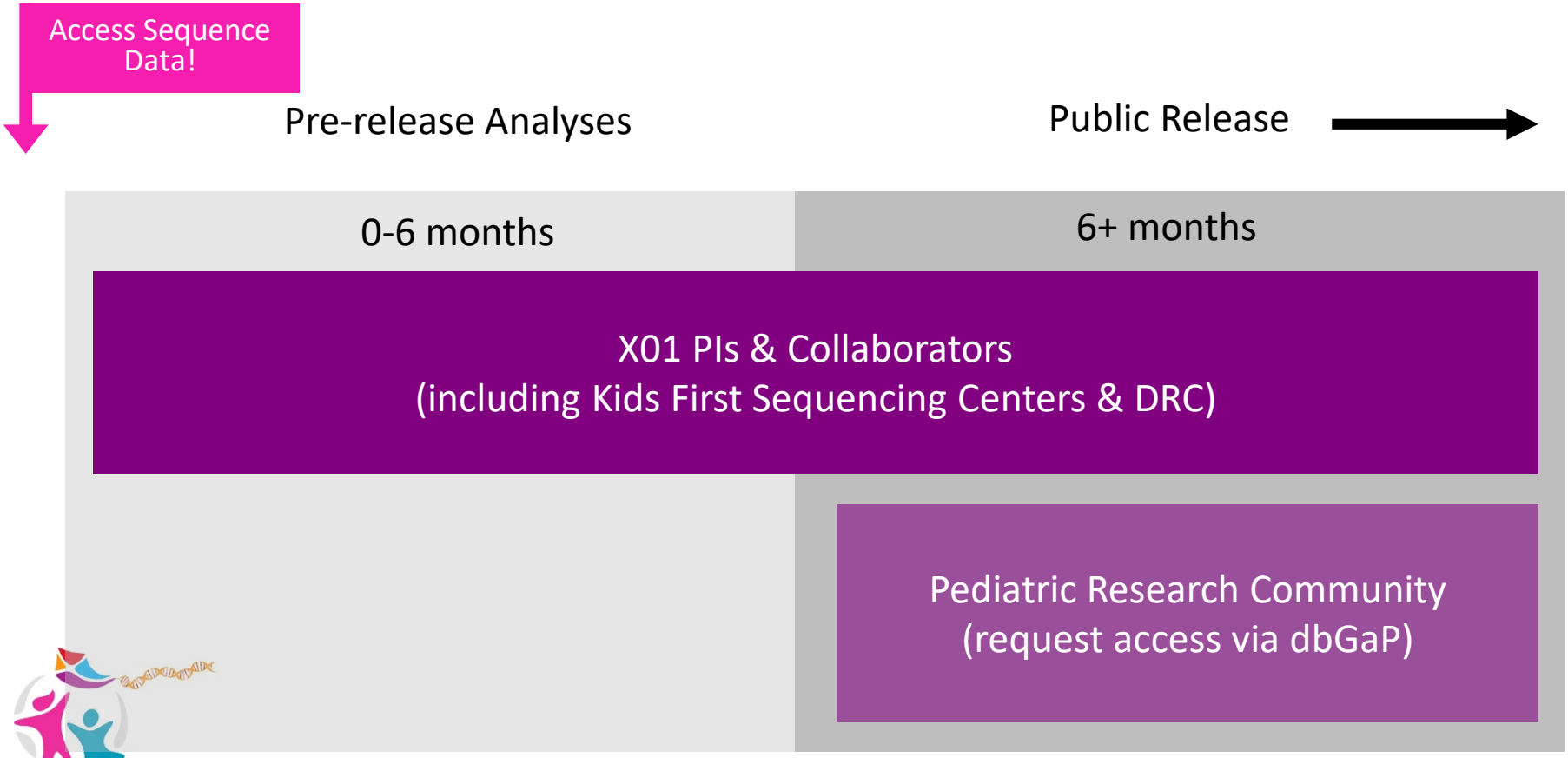
Expectations:

- Individual-level sequence and relevant phenotypic data are approved for deposition in a NIH-approved repository (e.g. dbGaP)
- Samples that are consented in a way that allows broad access and use, including combining and cross-analyzing datasets (General Research Use, Health/Medical/Biomedical), will be prioritized

See below and visit Kids First Genomic Data Sharing FAQs for more information

X01 Data Access & Six Month Pre-Release Period

- X01 investigators have six (6) months of proprietary access to the dataset before it is made available to the public.
- Pre-release period starts when the X01 team has access to all individual level sequence data (BAM/CRAM, VCFs)



Analysis Plans

Goal: Have investigators demonstrate that the proposed project has an adequate research design for genetic discovery, and that the X01 applicants are prepared to perform these analyses

Expectations:

- While Kids First recognizes that analytical power will increase when the data from each individual study is incorporated with other data that will be part of the Data Resource, it is important to demonstrate that the data will be useable on its own
- Consider partnering with other research teams with relevant expertise to develop the analysis plan

Study Design

Goal: Study design, sample size, and family structures are sufficient to lead to genetic discovery

Expectations:

- Large sample sizes preferred
  - Consider collaborating with other investigators to pool samples together
- Non-trio family designs: describe the number of probands and affected/unaffected family members proposed for sequencing

Clinical/Phenotypic Data

Goal: **Well-phenotyped data empowers analyses and informs how pathways/conditions overlap.**
The DRC will leverage existing community standards to harmonize clinical/phenotypic data which facilitates searching, analysis, and interoperability with other data efforts.

Expectations:

- Basic data elements are expected and deep phenotyping is preferred.
- Describe what clinical/phenotypic information is available and how these data will:
    1) support your proposed analysis
    2) contribute to the DRC to empower collaborative research

Program Balance

Goal: Broaden the diversity of both childhood cancer and structural birth defects datasets that are represented in the Data Resource

Expectation: Priority may be given to cohorts representing conditions not previously sequenced by Kids First (if many applications score well and meet other criteria)

Other Attachments

1) Institutional Certification (or provisional certification with data use limitations designations)
2) Sample Information
3) Clinical/Phenotypic Data
4) Family Structure (Optional)

fillable tables
(optional)

Institutional Certification: Steps

1) Download the current NIH Institutional (or Provisional) Certification template: *https://osp.od.nih.gov/scientific-sharing/institutional-certifications/*
   template was updated on November 1, 2018*
2) Fill out the first page, include all sites contributing samples for sequencing.
3) Provide the Institutional Certification to the IRB along with the participant consent forms for each site and any other pertinent information.
4) The IRB reviews the consent form(s) to determine the data use limitations (DULs) and/or DUL modifiers for each consent form.
   - **"General Research Use" with no modifiers is expected for individual-level data, unless specific uses are clearly prohibited in the participant consent**
   - **"Unrestricted" access is expected for genomic summary results unless the IRB provides a justification for designating the dataset as "sensitive"**
5) After IRB review, the Institutional Certification is signed by the appropriate officials and submitted to NIH.

Download a letter that explains these steps

Institutional Certification: Page 1

Date: [MM/DD/YYYY] 12/03/2018
Name of GPA: Jaime Guidry Auvil
Genomic Program Administrator
NCI, NIH, HHS
9000 Rockville Pike
Bethesda, MD 20892-7395

Re: Institutional Certification of [NAME OF INSTITUTION] to Accompany Submission of the Dataset from [ORIGINAL STUDY NAME[1]] for [PROJECT TITLE FOR DATA TO BE SUBMITTED] to an NIH-designated data repository.

Dear Jaime Guidry Auvil,

The submission of data to the NIH-designated data repository is being made with institutional approval from _____, along with appropriate institutional approvals from collaborating sites, as listed here:

[IF APPLICABLE ENTER COLLABORATING SITE NAMES HERE AND CLICK 'ADD TO LIST'] LIST OF COLLABORATING SITES

Add to list >> Clear list

The _____ hereby assures that submission of data from the study entitled _____ to an NIH-designated data repository meets the following expectations, as defined in the NIH Genomic Data Sharing Policy:

- The data submission is consistent, as appropriate, with applicable national, tribal, and state laws and regulations as well as relevant institutional policies.
- Any limitations on the research use of the data, as expressed in the informed consent documents, are delineated in the table on page 3.
- The identities of research participants will not be disclosed to NIH-designated data repositories.
- An Institutional Review Board (IRB), and/or Privacy Board, and/or equivalent body, as applicable, has reviewed the investigator's proposal for data submission and assures that:
  - The protocol for the collection of genomic and phenotypic data is consistent with 45 CFR Part 46;[2]
  - Data submission and subsequent data sharing for research purposes are consistent with the informed consent of study participants from whom the data were obtained;
  - Consideration was given to risks to individual participants and their families associated with data submitted to NIH-designated data repositories and subsequent sharing, including unrestricted access to genomic summary results;
  - To the extent relevant and possible, consideration was given to risks to groups or populations associated with submitting data to NIH-designated data repositories and subsequent sharing, including unrestricted access to genomic summary results; and
  - The investigator's plan for de-identifying datasets is consistent with the standards outlined in the NIH Genomic Data Sharing Policy (See section IV.C.1).

* Certification must be provided for all sites contributing samples. If more than one site is contributing samples, the primary site may submit one Institutional Certification indicating that they are providing certification on behalf of all collaborating sites. Alternatively, each site providing samples may provide its own Institutional Certification.

GPA: Jaime Guidry Auvil, NCI

List all sites contributing samples

Institutional Certification: Page 2

The individual-level data are to be made available through (check one)

- (•) **controlled-access** [3]
- ( ) **unrestricted access** [4]

If unrestricted access is marked, the data use limitations table on the following page(s) does not need to be completed.

NIH provides genomic summary results[5] (GSR) from most studies submitted to NIH-designated data repositories through unrestricted access. However, data from data sets considered to have particular 'sensitivities' related to individual privacy or potential for group harm (e.g., those with populations from isolated geographic regions, or with rare or potentially stigmatizing traits) may be designated as "sensitive" by

In such cases, "controlled-access" should be checked below and a brief explanation for the sensitive designation should be provided. GSR from any such data sets will only be available through controlled-access.

The genomic summary results (GSR) from this study are only to be made available through
☐ **controlled-access.**

Explanation if controlled-access was selected for GSR.

individual-level sequence data are expected to be "controlled-access", unless consent allows for unrestricted access

Keep unchecked for "unrestricted" access to **genomic summary results** unless the IRB provides a justification for designating the dataset as "sensitive"

31

Institutional Certification: Page 3

NIH expects the submitting institution(s) to select one of the three standard Data Use Limitations (DULs) for appropriate secondary use, or, if necessary, create a customized DUL. DULs are developed based on the original informed consent of the participant(s).

Data Use Limitations

General Research Use	GRU	Use of the data is limited only by the terms of the Data Use Certification: these data will be added to the dbGaP Collection.
Health/Medical/Biomedical	HMB	Use of the data is limited to health/medical/biomedical purposes, does not include the study of population origins or ancestry.
Disease-specific [list disease]	DS	Use of the data must be related to the specified disease.
Other		[ENTER CUSTOMIZED TEXT, IF APPLICABLE]

Additional modifiers to the standard DULs (e.g., Not-for-profit Use On
basis in the informed consent from the participants or in special knowle

"General Research Use" with no modifiers is expected for individual-level data, unless specific uses are clearly prohibited

Data Use Limitation Modifiers (Optional)

IRB Approval Required	IRB	Requestor must provide documentation of local IRB approval.
Publication Required	PUB	Requestor agrees to make results of studies using the data available to the larger scientific community.
Collaboration Required	COL	Requestor must provide a letter of collaboration with the primary study investigator(s).
Not-for-profit Use Only	NPU	Use of the data is limited to not-for-profit organizations.
Methods	MDS	Use of the data includes methods development research (e.g., development and testing of software or algorithms).
Genetic Studies Only	GSO	Use of the data is limited to genetic studies only.

Using the tables above, please indicate in the table below the consent group(s) for each collaborating study site. Use one row per consent group.

Collaborating Site Name	Data Use Limitation	Data Use Limitation Modifiers (optional)
Eg: Cold Cohort Study	*Health/Medical/Biomedical*	IRB ☐ PUB ☐ COL ☐ NPU ☐ MDS ☐ GSO ☐
Eg: Cold Cohort Study	*Disease Specific Research [Lung Cancer]*	IRB ☐ PUB ☐ COL ☐ NPU ☒ MDS ☐ GSO ☐
	General Research Use	IRB ☐ PUB ☐ COL ☐ NPU ☐ MDS GSO
	Select consent group title	IRB ☐ PUB ☐ COL ☐ NPU ☐ MDS GSO
	Select consent group title	IRB ☐ PUB ☐ COL ☐ NPU ☐ MDS GSO

The following data use limitations and modifiers limit broad data access and impede the ability of the Kids First program to accomplish its goals

- **Disease Specific Consent Group:** When data use is restricted to a specific disease area, the data cannot be combined with a dataset with a different disease specific data use limitation. Combining and cross-analyzing datasets are a primary goal of Kids First and therefore datasets that are consented for General Research Use and/or Health/Medical/Biomedical purposes will be prioritized over datasets restricted to Disease Specific use.
- **IRB modifier:** With this box checked, the Requester must provide documentation of a their local IRB's approval for the proposed research. We find that it is rare for consent language to include such a requirement and that this modifier is often included in error. As a reminder, every requester and their institution must agree to the terms of the Data Use Certification (DUC), which verifies that the requesting PI is accredited within the institution, the institution is aware of the project for which the PI is proposing to use the data, and that the Institution has all appropriate security measures in place to manage and maintain the controlled-access dataset(s) being retrieved. For a sample DUC, see: https://osp.od.nih.gov/wp-content/uploads/Model_DUC.pdf
- **COL modifier**: This box is checked when the consent form states that collaboration with the original/submitting investigator is required in order to use the dataset; therefore, the Requestor must provide a collaboration agreement document in order to be approved for access the dataset. This can limit the number of end-users who are able to use the dataset.

For more detail on DUL definitions:

https://osp.od.nih.gov/wp-content/uploads/NIH_PTC_in_Developing_DUL_Statements.pdf

Genomic Data Sharing Contacts

Jaime M. Guidry Auvil, Ph.D.
Genomic Program Administrator (GPA)
Director, NCI Office of Data Sharing
NCIOfficeofDataSharing@mail.nih.gov

Vivian Ota Wang, Ph.D.
Kids First Data Access Committee (DAC) Chair
Deputy Director, NCI Office of Data Sharing
KidsFirstDAC@nih.gov

General NIH Genomic Data Sharing questions: GDS@mail.nih.gov

Other Attachments

1) Institutional Certification (or provisional certification with description of data use limitations)
2) Sample Information
3) Clinical/Phenotypic Data
4) Family Structure (Optional)

fillable tables
(optional)

https://commonfund.nih.gov/kidsfirst/FAQ

Other Attachments: Fillable Table

Provisional Certification

1) Provisional Certification: Data Sharing and Data Use Limitations

If you provided a Provisional Institutional Certification, because you are unable to provide a full Institutional Certification, please describe the anticipated data use limitations based on the language of the consent form(s) signed by the participants in the proposed cohort. For a list of standard DULs and modifiers, please review the Institutional Certification template: https://osp.od.nih.gov/scientific-sharing/institutional-certifications or https://osp.od.nih.gov/wp-content/uploads/standard_data_use_limitations.pdf.

Site	**Data Use Limitation** (GRU, HMB, DS)	**Data Use Limitation Modifiers** (IRB, PUB, COL, NPU, MDS, GSO)

Other Attachments: Fillable Table

Sample Information

DNA (and RNA) tissue of origin	**Number of Samples**	**Extraction Method**	**Concentration**	**Quality (Metric used:** *[edit here to specify])*	**Method of Quantitation**	**Number of Samples Ready to Ship by August 2019**	**Number of Samples Ready to Ship by January 2020**
Blood							
Saliva or Buccal swab							
[other tissue, edit here to describe]. **Note: cell lines will not be accepted**							
Tumors or Affected Somatic Tissue							
DNA – Frozen Tissue							
RNA – Frozen Tissue							
DNA – Embedded Tissue							
RNA – Embedded Tissue							
Total							

*For tumor specimens or affected tissue samples, please also describe the fixation methods and the pathology review to which the specimens were subjected, separate from the table. For tumors, describe the percentage of tumor cells within the specimen used for DNA and/or RNA isolation and % necrosis.

Other Attachments: Fillable Table

Clinical/Phenotypic Data & Demographics

Available Phenotype or Clinical Information (for #3 Clinical, Phenotypic, and Demographic Data). Please edit or add to the table below to indicate what phenotype information is available for the case/proband, parents, and/or other family members. The information you list is intended to be shared through the Kids First Data Resource.

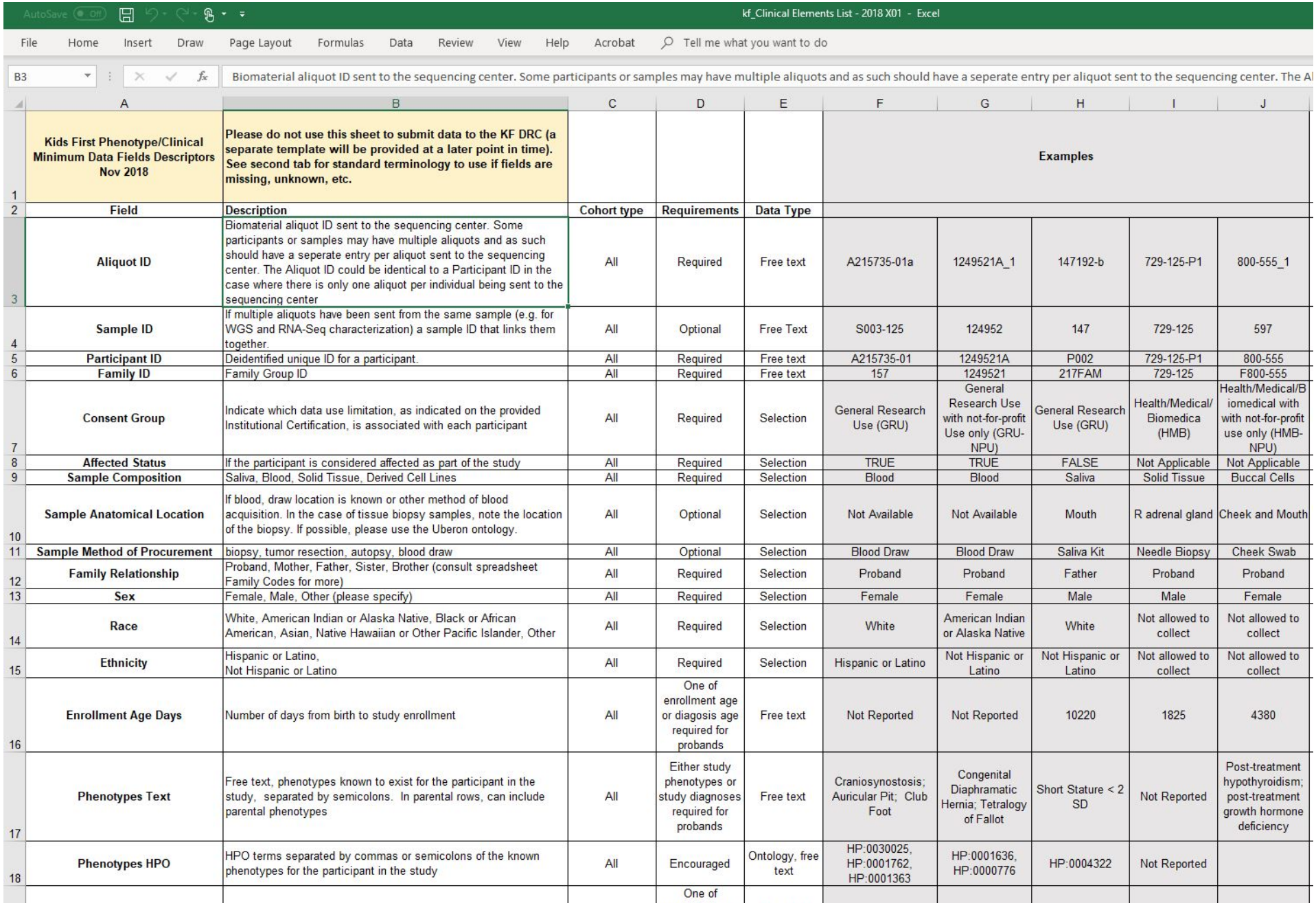
Demographics	Case/Proband/Affected	Unaffected family members/parents
o Age at enrollment or age at diagnosis		
o Other age information (age at specimen collection, age at death etc.…)		
o Sex		
o Race		
o Hispanic ethnicity		
o List any other demographic information:		

Clinical information (e.g., diagnoses, type of birth defect, primary tumor type, vital status, age at last know vital status, treatment information).		
	Case/Proband/Affected	Unaffected family members/parents
List the variables:		
Are electronic health records available?		

Other phenotypic information (e.g., other phenotypic measurements that may be related to the primary outcome)		
	Case/Proband/Affected	Unaffected family members/parents
List the variables		

Family medical history (e.g., family history of birth defects, family history of cancer)		
	Case/Proband/Affected	Unaffected family members/parents
List the variables:		

Biospecimen & Phenotypic Data Elements



kf_Clinical Elements List - 2018 X01 - Excel

File Home Insert Draw Page Layout Formulas Data Review View Help Acrobat Tell me what you want to do

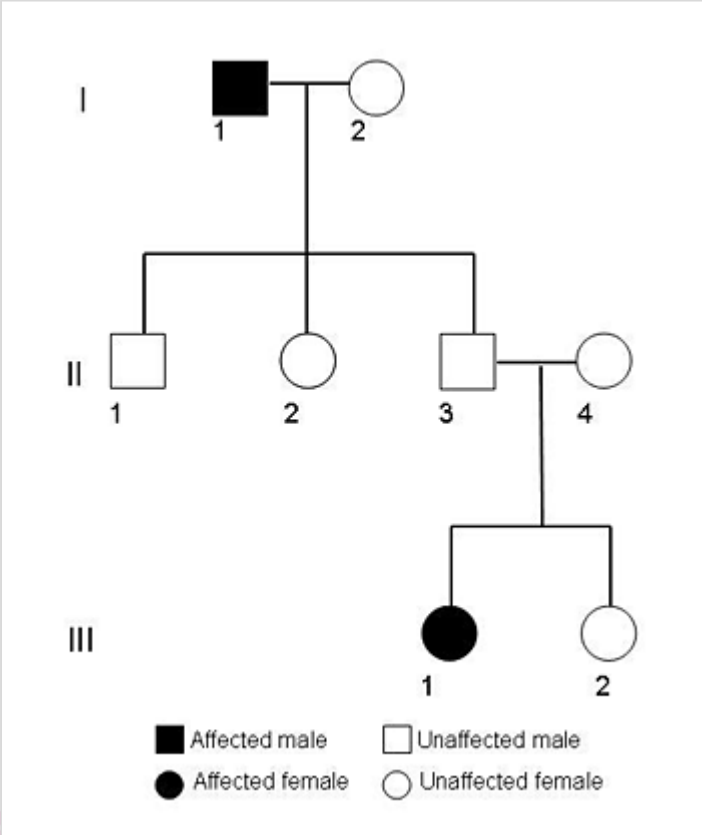
B3: Biomaterial aliquot ID sent to the sequencing center. Some participants or samples may have multiple aliquots and as such should have a seperate entry per aliquot sent to the sequencing center. The Al

	A	B	C	D	E	F	G	H	I	J
1	**Kids First Phenotype/Clinical Minimum Data Fields Descriptors Nov 2018**	**Please do not use this sheet to submit data to the KF DRC (a separate template will be provided at a later point in time). See second tab for standard terminology to use if fields are missing, unknown, etc.**				**Examples**				
2	**Field**	**Description**	**Cohort type**	**Requirements**	**Data Type**					
3	**Aliquot ID**	Biomaterial aliquot ID sent to the sequencing center. Some participants or samples may have multiple aliquots and as such should have a seperate entry per aliquot sent to the sequencing center. The Aliquot ID could be identical to a Participant ID in the case where there is only one aliquot per individual being sent to the sequencing center	All	Required	Free text	A215735-01a	1249521A_1	147192-b	729-125-P1	800-555_1
4	**Sample ID**	If multiple aliquots have been sent from the same sample (e.g. for WGS and RNA-Seq characterization) a sample ID that links them together.	All	Optional	Free Text	S003-125	124952	147	729-125	597
5	**Participant ID**	Deidentified unique ID for a participant.	All	Required	Free text	A215735-01	1249521A	P002	729-125-P1	800-555
6	**Family ID**	Family Group ID	All	Required	Free text	157	1249521	217FAM	729-125	F800-555
7	**Consent Group**	Indicate which data use limitation, as indicated on the provided Institutional Certification, is associated with each participant	All	Required	Selection	General Research Use (GRU)	General Research Use with not-for-profit Use only (GRU-NPU)	General Research Use (GRU)	Health/Medical/ Biomedica (HMB)	Health/Medical/Biomedical with with not-for-profit use only (HMB-NPU)
8	**Affected Status**	If the participant is considered affected as part of the study	All	Required	Selection	TRUE	TRUE	FALSE	Not Applicable	Not Applicable
9	**Sample Composition**	Saliva, Blood, Solid Tissue, Derived Cell Lines	All	Required	Selection	Blood	Blood	Saliva	Solid Tissue	Buccal Cells
10	**Sample Anatomical Location**	If blood, draw location is known or other method of blood acquisition. In the case of tissue biopsy samples, note the location of the biopsy. If possible, please use the Uberon ontology.	All	Optional	Selection	Not Available	Not Available	Mouth	R adrenal gland	Cheek and Mouth
11	**Sample Method of Procurement**	biopsy, tumor resection, autopsy, blood draw	All	Optional	Selection	Blood Draw	Blood Draw	Saliva Kit	Needle Biopsy	Cheek Swab
12	**Family Relationship**	Proband, Mother, Father, Sister, Brother (consult spreadsheet Family Codes for more)	All	Required	Selection	Proband	Proband	Father	Proband	Proband
13	**Sex**	Female, Male, Other (please specify)	All	Required	Selection	Female	Female	Male	Male	Female
14	**Race**	White, American Indian or Alaska Native, Black or African American, Asian, Native Hawaiian or Other Pacific Islander, Other	All	Required	Selection	White	American Indian or Alaska Native	White	Not allowed to collect	Not allowed to collect
15	**Ethnicity**	Hispanic or Latino, Not Hispanic or Latino	All	Required	Selection	Hispanic or Latino	Not Hispanic or Latino	Not Hispanic or Latino	Not allowed to collect	Not allowed to collect
16	**Enrollment Age Days**	Number of days from birth to study enrollment	All	One of enrollment age or diagosis age required for probands	Free text	Not Reported	Not Reported	10220	1825	4380
17	**Phenotypes Text**	Free text, phenotypes known to exist for the participant in the study, separated by semicolons. In parental rows, can include parental phenotypes	All	Either study phenotypes or study diagnoses required for probands	Free text	Craniosynostosis; Auricular Pit; Club Foot	Congenital Diaphramatic Hernia; Tetralogy of Fallot	Short Stature < 2 SD	Not Reported	Post-treatment hypothyroidism; post-treatment growth hormone deficiency
18	**Phenotypes HPO**	HPO terms separated by commas or semicolons of the known phenotypes for the participant in the study	All	Encouraged	Ontology, free text	HP:0030025, HP:0001762, HP:0001363	HP:0001636, HP:0000776	HP:0004322	Not Reported	
				One of						

Other Attachments: Pedigree or Table

Describe Family structures (proband-parent dyads, proband-parent-sibling quads, multiplex families, consanguineous families)

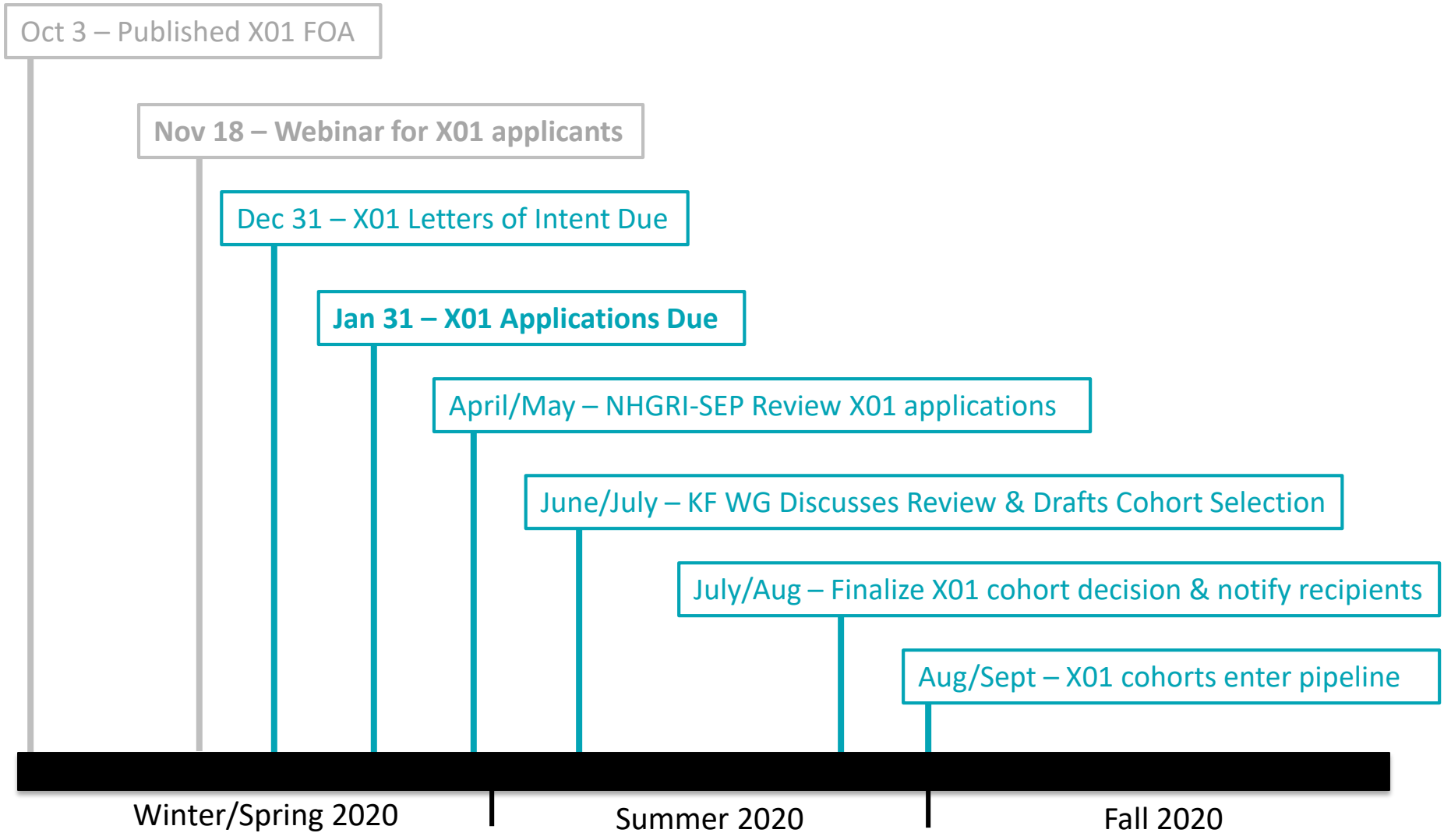
- How many samples per family? How many are affected/unaffected?



Family type	Number of families	Total Germline Samples
Proband/Child + Parents (unaffected) Trios	XX	XX affected XX unaffected
Proband + 1 affected FDR + [Unaffected FDRs]	XX	XX affected XX unaffected
Proband + 2 affected FDR + [Unaffected FDRs]	XX	XX affected XX unaffected
Total	XXX	XXX

FDR= First Degree Relative

2020 X01 Timeline



Agenda

- **12-12:25pm.** PAR-19-390 - ***Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)*** **–** Valerie Cotton, NICHD
- **12:25-12:30pm.** PAR-19-375- ***Small Research Grants for Analyses of Gabriella Miller Kids First Pediatric Research Data (R03 Clinical Trial Not Allowed)*** – James Coulombe, NICHD
- **12:30-12:35pm.** Common Fund FOA – Marie Nierras
- **12:35-12:45pm.** ORIP FOAs – Sige Zou & Oleg Mirochnitchenko
- **12:45-12:55pm.** NIDCR FOAs – Emir Khatipov
- **12:55-1pm.** Questions & Additional FOAs

Small Research Grants for Analyses of Gabriella Miller Kids First Pediatric Research Data

(R03 - Clinical Trial Not Allowed)

PAR-19-375

Purpose: support analyses of Kids First X01 datasets and appropriate tools development

- NICHD, NCI, NHLBI, NIAAA, and NIDCR
- Standard Receipt Dates (after Open Date): Feb 2020
- Combined direct cost budget for the two-year project period may not exceed $200,000
- Contact IC representative or James Coulombe (coulombej@mail.nih.gov)

Small Research Grants for Analyses of Gabriella Miller Kids First Pediatric Research Data

(R03 - Clinical Trial Not Allowed)

PAR-19-375

FOA Updates

- Data and Resource Sharing Plans:
  - "data…, tools, workflows, and/or pipelines ***created*** or ***used*** …will be provided to the Kids First Data Resource Center to be shared with the wider scientific community… in ***a timely manner*** that would enable other researchers to replicate and build on the analyses for future research efforts."
  - For applications that aim to co-analyze Kids First X01 data with non-Kids First genomic datasets, describe:
    - the database through which the non-KF data are accessible, or
    - ability & willingness to submit the non-KF sequence data to an NIH-approved repository (e.g., dbGaP)

Small Research Grants for Analyses of Gabriella Miller Kids First Pediatric Research Data

(R03 - Clinical Trial Not Allowed)

PAR-19-375

- Are "junior" investigators eligible? Yes!
- If your institution is willing to submit your application, you are eligible.
- For R03s there are no special considerations for New or Early Stage Investigators.
- However, R03s are a great mechanism for producing preliminary data that can lead to other applications.

Agenda

- **12-12:25pm.** PAR-19-390 - ***Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)*** **–** Valerie Cotton, NICHD
- **12:25-12:30pm.** PAR-19-375- ***Small Research Grants for Analyses of Gabriella Miller Kids First Pediatric Research Data (R03 Clinical Trial Not Allowed)*** – James Coulombe, NICHD
- **12:30-12:35pm.** Common Fund FOA – Marie Nierras
- **12:35-12:45pm.** ORIP FOAs – Sige Zou & Oleg Mirochnitchenko
- **12:45-12:55pm.** NIDCR FOAs – Emir Khatipov
- **12:55-1pm.** Questions & Additional FOAs

Pilot Projects Enhancing Utility and Usage of Common Fund Data Sets

(R03 Clinical Trial Not Allowed)

RFA-RM-19-012

- **Purpose**: Small research (R03) grants provide flexibility for initiating discrete, well-defined projects that can be completed in one year, for up to $200,000 in direct costs
- Examples of research that will be supported:
  - Conducting pilot or feasibility studies based on analyses across Common Fund datasets;
  - Building synthetic cohorts, combining and comparing datasets;
  - Developing research methods, or analytic tools to support data visualization, harmonization and integration;
  - Curating and or annotating genomic information in the datasets;
  - Collecting additional phenotypic or clinical data to enhance datasets.

– Contact KF, or Ananda Roy (ananda.roy@nih.gov)

Agenda

- **12-12:25pm.** PAR-19-390 - ***Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)*** **–** Valerie Cotton, NICHD
- **12:25-12:30pm.** PAR-19-375- ***Small Research Grants for Analyses of Gabriella Miller Kids First Pediatric Research Data (R03 Clinical Trial Not Allowed)*** – James Coulombe, NICHD
- **12:30-12:35pm.** Common Fund FOA – Marie Nierras
- **12:35-12:45pm.** ORIP FOAs – Sige Zou & Oleg Mirochnitchenko
- **12:45-12:55pm.** NIDCR FOAs – Emir Khatipov
- **12:55-1pm.** Questions & Additional FOAs

ORIP

OFFICE OF RESEARCH INFRASTRUCTURE PROGRAMS

Division of Comparative Medicine

ORIP Resource-Related Programs

Sige Zou, PhD and Oleg Mirochnitchenko, PhD
Division of Comparative Medicine
Office of Research Infrastructure Programs
Division of Program Coordination, Planning, and Strategic Initiatives
Office of the Director

NIH National Institutes of Health
Office of Research Infrastructure Programs

Office of Research Infrastructure Programs

Mission:

Infrastructure and Resources for Innovation

Division of Comparative Medicine

- Centers and research resources
- Research project grants
- Training and career development programs for veterinarian-scientists

Division of Construction & Instruments

- Construction awards
- Shared instrumentation grant and high-end instrumentation programs (S10)

SBIR/STTR Programs

https://orip.nih.gov/

Division of Comparative Medicine

- ORIP's Strategic Plan:
  - Development and enhancement of models of human disease as well as expansion and accessibility of these models
  - Provide better models of human disease conditions of interest to multiple NIH ICs
- Major Types of Activities to Support Animal Models of Disease
  - Center Grants (e.g. P51, P40, and U42)
  - Resource-Related Research Project Grants (e.g. R24)
  - Research Project Grants (e.g. R21)
- Requirements of Grant Applications:
  - Demonstrate a need for a resource by the broad research community
  - Applicable to the interests of multiple NIH ICs

Research Project Grants (R21)

Funding Opportunity Title (PAR-19-369):

- Development of Animal Models and Related Biological Materials for Research (R21 Clinical Trial Not Allowed)

Purpose:

- Encourages innovative research to develop, characterize, and improve animal models, biological materials, and technologies

General Characteristics:

- Support conceptual stages of project development
- No preliminary data required
- Cannot be renewed

Topics of Interest for ORIP:

- Development or characterization of animal models
- Development of novel technologies for improving animal models
- Complementary approaches to the use of animals, such as animal-tissue-on-chip models
- Informatics and artificial intelligence tools for deep phenotyping

Resource-Related Research Projects Grants (R24)

Funding Opportunity Title (RFA-OD-19-027):

- Resource-Related Research Projects for Development of Animal Models and Related Materials (R24 Clinical Trials Not-Allowed)

Purpose:

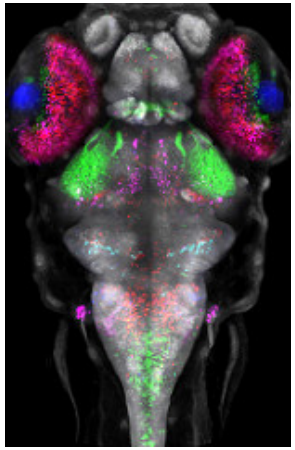
- Develop, characterize, or improve animal models
- Improve diagnosis and control of disease of laboratory animal

General Characteristics:

- Used to provide a substantial amount of resources to research projects or to enhance research infrastructure
- Cost recovery is not required

Topics of Interest for ORIP:

- Mutant or transgenic animal models
- Antibodies, genetic resources or other reagents
- Information resources, such as cellular phenotypes
- Animal resources for supporting trans-NIH initiatives



Animal & Biological Material Resource Centers (P40)

Funding Opportunity Title (PAR-17-006):

- Animal and Biological Material Resource Centers (P40)

Purpose:

- Provide support for special colonies of laboratory animals and animal-related models, as well as other resources such as informatics tools, reagents, cultures (cells, tissues, and organs) and genetic stocks that serve the biomedical research community in a variety of research areas on a local, regional, national and international basis.

Animal & Biological Material Resource Centers (P40)

General Characteristics:

- As part of ORIP's trans-NIH emphasis, Animal and Biological Material Resource Centers to be developed must address the research interests of multiple NIH Institutes and Centers
- Applications must demonstrate a wide community need for the proposed Resource Centers
- Animal and Biological Material Resource Centers must be available and utilized by investigators on a local, regional, and national basis
- These Resource Centers should ensure the quality and welfare of distributed animals and supply expertise to guide reliable studies
- Institution submitting the application must be committed to the Resource Center being proposed
- Growth of the Resource Centers should result from Program Income
- Applications must include a marketing plan, community outreach strategies and approaches for tracking metrics
- Resource Centers are expected to register their catalogs with current resource tagging and identification initiatives such as FORCE 11

Current Resource Centers Portfolio

Biological Materials and Informatics, Other

- National Natural Toxins Research Center
- Referral Center for Animal Models of Human Genetic Disease

- Nonhuman Primate Reagent Resource
- *Drosophila* Genomics Resource Center
- Center for Neuroanatomy with Neurotropic Viruses
- *Caenorhabditis* Genetics Center

Primate

- Squirrel Monkey Breeding and Research Resource
- Vervet Research Colony
- Specific Pathogen Free Baboon Research Resource
- Caribbean Primate Research Center

Rodent

- National Gnotobiotic Roden Resource
- Rat Resource and Research Center Special Mouse Strains Resource
- Resource for Rat Genetic Models of Aerobic Capacity

Amphibian

- National *Xenopus* Resource Center
- *Ambystoma* Genetic Stock Center

Fish

- Zebrafish International Resource Center

Invertebrate

- Bloomington *Drosophila* Stock Center
- National Resource for *Aplysia*
- Resource Center for *Tetrahymena*

Gabriella Miller Kids First Pediatric Research Program (Kids First)

- P40 supported facilities – resources for animal models
- Several P40 Centers provide expertise and services to the community
- P40 Centers will be happy to acquire and re-distribute models created by Kids First
- P40 FOA – create your own resource

Summary

ORIP supports development, enhancement and distribution of animal models of interest to multiple NIH ICs

Scientific Contacts:

- R21 (PAR-19-369): Development of Animal Models and Related Biological Materials
  - Sige Zou, PhD; Telephone: 301-435-0749; Email: sige.zou@nih.gov
- R24 (RFA-OD-19-027): Resource-Related Research Projects for Development of Animal Models and Related Materials
  - Stephanie Murphy, VMD, PhD; Telephone: 301-451-7818; Email: stephanie.murphy@nih.gov
  - Sige Zou, PhD; Telephone: 301-435-0749; Email: sige.zou@nih.gov
- P40 (PAR-17-006): Animal and Biological Material Resource Centers
  - Oleg Mirochnitchenko, PhD; Telephone: 301-435-0748; Email: oleg.mirochnitchenko@nih.gov

Questions?

Agenda

- **12-12:25pm.** PAR-19-390 - ***Discovery of the Genetic Basis of Childhood Cancers and of Structural Birth Defects: Gabriella Miller Kids First Pediatric Research Program (X01 Clinical Trial Not Allowed)*** **–** Valerie Cotton, NICHD
- **12:25-12:30pm.** PAR-19-375- ***Small Research Grants for Analyses of Gabriella Miller Kids First Pediatric Research Data (R03 Clinical Trial Not Allowed)*** – James Coulombe, NICHD
- **12:30-12:35pm.** Common Fund FOA – Marie Nierras
- **12:35-12:45pm.** ORIP FOAs – Sige Zou & Oleg Mirochnitchenko
- **12:45-12:55pm.** NIDCR FOAs – Emir Khatipov
- **12:55-1pm.** Questions & Additional FOAs

NIDCR Funding Opportunities

Emir Khatipov, Ph.D., Director,
Bioinformatics, Computational Biology
and Data Sciences Program
Translational Genomics Research Branch,
National Institute for Dental and Craniofacial Research

November 21, 2019

National Institute of Dental and Craniofacial Research

NIDCR Program Announcements (PARs)
Data Analysis

FOA	Title	Scope	Open date
PAR-20-045	NIDCR Research Grants for Analyses of Existing Genomics Data (**R01** Clinical Trial Not Allowed)	1) Research addressing questions relevant to human dental, oral, or craniofacial (DOC) conditions or traits through analysis of existing and publicly available genomics data using statistical and computational approaches. 2) Data analysis for each project using existing and/or novel methods to be developed in the same project, including machine learning-based methods (ML). 3) Experimental or *in silico* work is required to validate data analysis results, or to validate a newly developed analytic method.	1/05/2020
PAR-20-046	NIDCR Small Research Grants for Analyses of Existing Genomics Data (**R03** Clinical Trial Not Allowed)	1) Same as above 2) Same as above 3) Experimental validation of data analysis results or new methods may be proposed, but the focus of the project should be on analysis of existing data.	1/16/2020

NIDCR Notice of Special Interest (NOSI)

FOA	Title	Scope	Mechanism
NOT-DE-19-016 Application period: January 7, 2020 through January 8th, 2022	Notice of Special Interest (NOSI) of NIDCR in Supporting Discovery, Characterization, and Mechanistic Study of Genetic Variants Underlying Dental, Oral, and Craniofacial Diseases and Conditions.	Projects targeting human DOC phenotypes that propose specific aims in each of the following categories: 1) discovery of candidate causal genetic variants, 2) functional characterization of identified variants, and 3) mechanistic studies.	**R01**: parent FOA PA-19-056, Indicate this NOSI in the application

NIDCR Program Announcements (PARs)
(partnering with NICHD and NIEHS)

FOA	Title	Scope	Open date
PAR-19-292	Mechanistic Studies of Gene-Environment Interplay in Dental, Oral, Craniofacial, and Other Diseases and Conditions (**R01** Clinical Trial Not Allowed)	Applications that use animal models, in vitro systems, or ex vivo approaches to conduct mechanistic investigation of the interplay of genes/gene networks and environmental factors in dental, oral, craniofacial (DOC), and other diseases and conditions.	9/05/2019
PAR-19-293	Development of Novel and Robust Systems for Mechanistic Studies of Gene-Environment Interplay in Dental, Oral, Craniofacial, and Other Diseases and Conditions (**R21** Clinical Trial Not Allowed)	To develop novel and robust experimental systems that offer approaches complementary to human epidemiologic or in vivo studies to facilitate mechanistic investigation of gene-environment interplay in DOC and other diseases and conditions	9/16/2019

Q & A

- To ask public questions, use the **Q&A** bar (right side of your screen).
- You can ask also use the “chat”  service to send private messages to the host or presenters throughout the webinar.

FOAs for Data Analyses

- "**Kids First R03-PAR**": https://grants.nih.gov/grants/guide/pa-files/PAR-19-375.html
- **NIH "Parent" R03**: https://grants.nih.gov/grants/guide/pa-files/PA-19-052.html
- **NIH "Parent" R01**: https://grants.nih.gov/grants/guide/pa-files/PA-19-056.html
- **NCI:** ***Secondary Analysis and Integration of Existing Data to Elucidate the Genetic Architecture of Cancer Risk and Related Outcomes*** (Contact: Melissa Rotunno, Ph.D rotunnom@mail.nih.gov)
  - R01: https://grants.nih.gov/grants/guide/pa-files/PA-17-239.html
  - R21: https://grants.nih.gov/grants/guide/pa-files/PA-17-243.html
- **NIDCR:** ***Notice of Special Interest (NOSI) of NIDCR in Supporting Discovery, Characterization, and Mechanistic Study of Genetic Variants Underlying Dental, Oral, and Craniofacial Diseases and Conditions*** https://grants.nih.gov/grants/guide/notice-files/NOT-DE-19-016.html
- ***NIDCR Research Grants for Analyses of Existing Genomics Data (R01)*** https://grants.nih.gov/grants/guide/pa-files/PAR-19-390.html
- ***NIDCR Small Research Grants for Analyses of Existing Genomics Data (R03)*** https://grants.nih.gov/grants/guide/pa-files/PAR-20-046.html

FOAs for Variant Validation

- **ORIP:** ***Development of Animal Models and Related Biological Materials for Research (R21 Clinical Trial Not Allowed)***
  https://grants.nih.gov/grants/guide/pa-files/PAR-19-369.html
- **ORIP:** ***Resource-Related Research Projects for Development of Animal Models and Related Materials (R24 Clinical Trials Not-Allowed)***
  https://grants.nih.gov/grants/guide/rfa-files/RFA-OD-19-027.html
- **NIDCR:** ***Mechanistic Studies of Gene-Environment Interplay in Dental, Oral, Craniofacial, and Other Diseases and Conditions (R01 Clinical Trial Not Allowed).*** https://grants.nih.gov/grants/guide/pa-files/PAR-19-292.html
- **NIDCR:** ***Development of Novel and Robust Systems for Mechanistic Studies of Gene-Environment Interplay in Dental, Oral, Craniofacial, and Other Diseases and Conditions (R21 Clinical Trial Not Allowed).***
  https://grants.nih.gov/grants/guide/pa-files/PAR-19-293.html
- **NHGRI:** ***Novel Approaches for Relating Genetic Variation to Function and Disease (R01 Clinical Trial Not Allowed)***
  https://grants.nih.gov/grants/guide/pa-files/pa-18-868.html
- To pursue collaborations with the Knockout Mouse Phenotyping Program (KOMP2), contact: KidsFirstKOMP@nih.gov

Thank You!

To receive updates about future Kids First opportunities, sign up for the listserv:
https://list.nih.gov/cgi-bin/wa.exe?SUBED1=KIDSFIRST&A=1

Gabriella Miller Kids First
PEDIATRIC RESEARCH PROGRAM

X01 Helpful Links

- https://grants.nih.gov/grants/guide/pa-files/PAR-19-390.html
- https://commonfund.nih.gov/kidsfirst/faq
- https://kidsfirstdrc.org/
- https://portal.kidsfirstdrc.org
- https://osp.od.nih.gov/scientific-sharing/institutional-certifications/

Examples of Research Project Grants (R21)

Image-guided robot for high-throughput microinjection of *Drosophila* embryos:

- Develop a computer vision guided robotic microinjector for high-throughput microinjection

Enhancing CRISPR-Cas for disease modeling in *Xenopus*:

- Examine a CRISPR technique for its efficiency in generating mutations in *Xenopus*

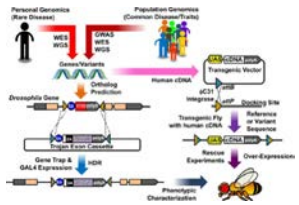
Genetic Modification to Harness the Regenerative Power of the African Spiny Mouse:

- Develop a gene knockout technique in *Acomys*

Germ cell preservation of immunodeficient pigs utilizing embryo complementation approach:

- Developing a standardized procedure to preserve germ cells from any type of immunodeficient pigs

Examples of Resource-Related Research Projects Grants (R24)

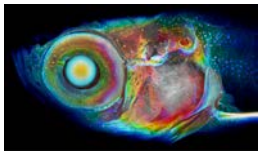


A Comprehensive Human cDNA Library For Functional Gene Replacement in *Drosophila*:

- Generate human cDNA library and related transgenic flies to facilitate clinical genomics interpretation

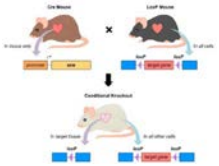
Research Resources for Model Amphibians:

- Develop genomic and bioinformatic resources for the Mexican axolotl (*Ambystoma mexicanum*)



Groundwork for a Synchrotron MicroCT Imaging Resource for Biology:

- Enable high-throughput, quantitative, 3D histological phenotyping of whole, millimeter-scale animals



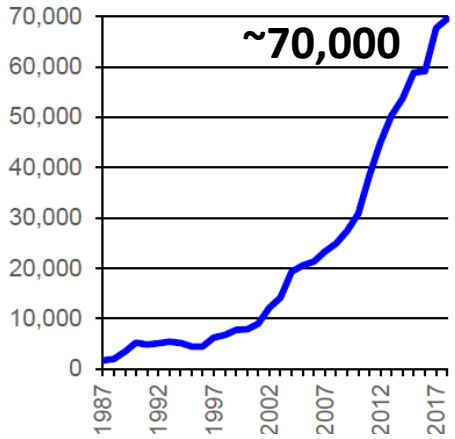
CRE Driver Strain Resources:

- A comprehensive set of well-characterized Cre Driver mouse lines and related information resources

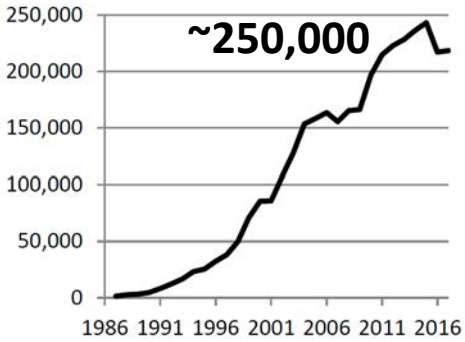
Bloomington *Drosophila* Stock Center (P40 OD018537)
Kevin R. Cook, Indiana University, IN

Funded by: ORIP (Primary), NIGMS, NICHD, NINDS, HHMI

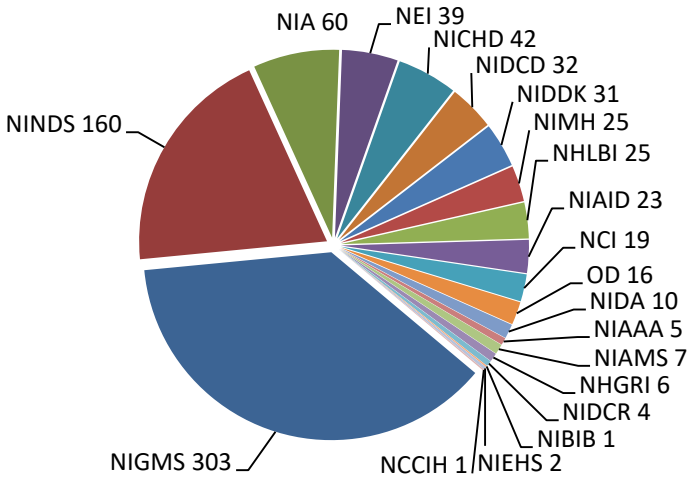
Stocks in Collection



Samples Shipped Annually

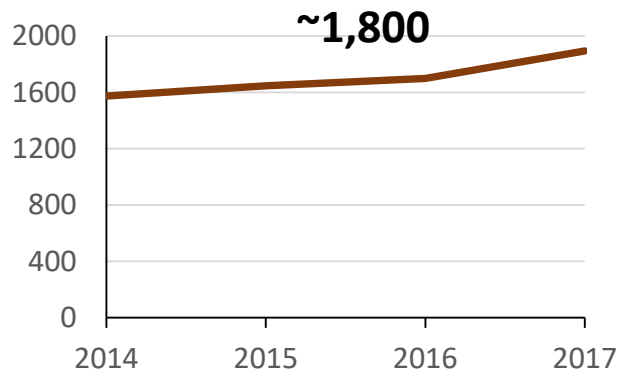


The Center collects, maintains and distributes genetically defined strains of *Drosophila* with significant research value



Support >1,000 NIH grants

Publications Citing BDSC Annually

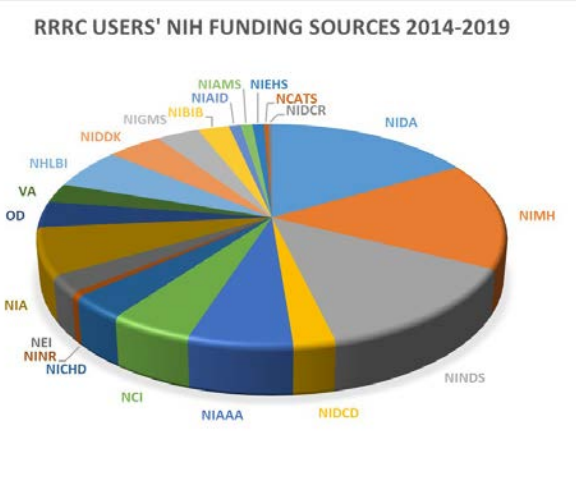


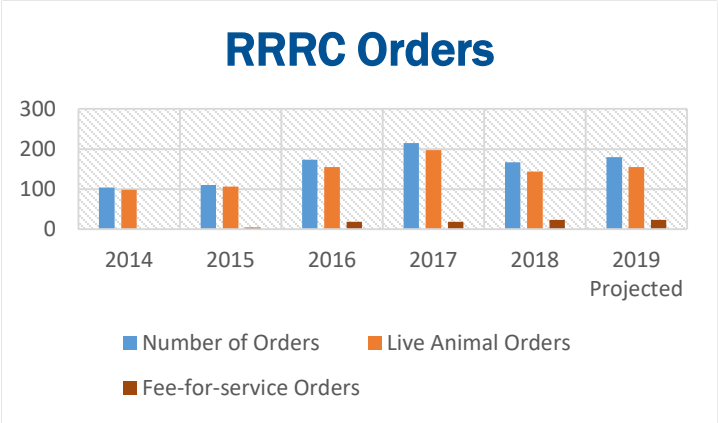
NIH National Institutes of Health
Office of Research Infrastructure Programs

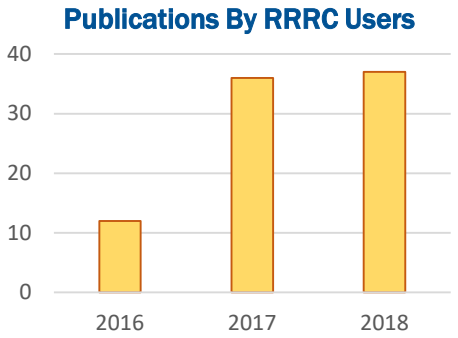
Rat Resource and Research Center (RRRC, P40 OD011062)
Elizabeth Bryda, University of Missouri

Current holdings: >450 unique rat strains/stocks and 6 embryonic stem cell lines

The RRRC provides a unique repository service to the biomedical community for importing, storing and distributing valuable rat strains and providing rat-related services







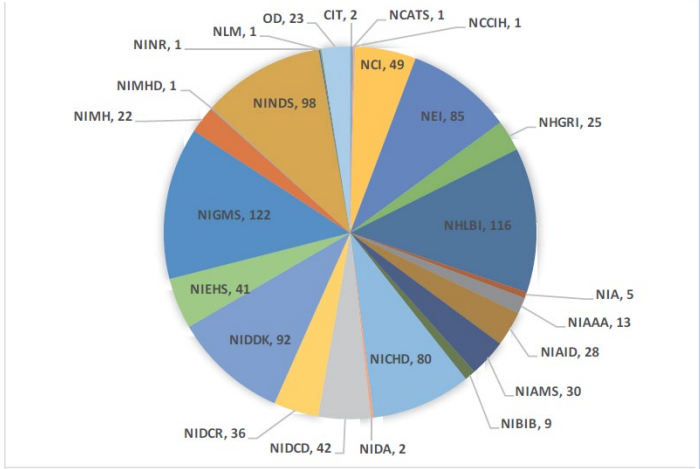
Additional services: unique cryopreservation approaches (ICSI), genotyping/genetic characterization, rederivation, genome editing (CRISPR/Cas9) for model creation, tissue/sample isolation, phenotyping, colony management, microbiota characterization

NIH National Institutes of Health
Office of Research Infrastructure Programs

Zebrafish International Resource Center (P40 OD011021)
Monte Westerfield, University of Oregon, OR

The Zebrafish International Resource Center is a zebrafish repository that provides animals, materials and services to the research community for more than 20 years

Funded by ORIP and NICHD



- The only national repository for zebrafish genetic stocks (>11,600 lines and 39,000 alleles) and research materials (antibodies, cDNA/EST, etc.)
- Provides the highest quality animal lines raised under stringent health monitoring
- Develops, characterizes, maintains, cryopreserves and distributes both wild-type strains and mutant zebrafish
- Provides pathology and consultation services
- Develops diagnostic platforms to screen for common pathogens that are threats to laboratory zebrafish

Resources and services to PIs supported by 23 NIH Institutes

Last year, ZIRC distributed 114,555 animals to 530 laboratories (94% NIH supported)